



## AMENDMENTS TO SPECIFICATION

Please delete paragraph [01] on page 1.

Please replace paragraph [66] on page 23 with the following amended paragraph:

[66] The BLAST algorithm is well suited for determining percent sequence identity and sequence similarity. The BLAST algorithm is described in Altschul et al., J Mol. 215:403-410, (1990), the entire contents of which are herein incorporated by reference for all purposes. Several software programs incorporating the BLAST algorithm are publicly available through the National Center for Biotechnology Information (NCBI) (<http://www.ncbi.nlm.nih.gov/>). These programs include the blastp, blastn, blastx, tblastn, tblastx, and PSI-blast software programs. Due to codon wobble or species differences, more informative homologies can be found by comparing the predicted protein sequence of a DNA query sequence to a protein sequence database. For this task, the Smith-Waterman or PSI-BLAST algorithms may be used. Similarly, for weak homologs, functional domains of proteins may be discerned by Smith-Waterman, HMM or Emotif algorithms. Software for performing HMM and Smith-Waterman analysis can be obtained from a variety of public sources (e.g. ~~<http://hmmerr.wustl.edu/>~~; ~~<http://www.stanford.edu/~sntaylor/bioc218/final.htm#Appendix>~~) and/or from vendors that sell accelerated computer hardware to rapidly process large batches of sequences (e.g. Paracel, Pasadena, CA or TimeLogic, Crystal Bay, NV). Software for EMotif/Ematrix can be obtained from sources such as the Brutlag Bioinformatics Group, Stanford University, Stanford, CA.